```
CLUSTAL 2.1 multiple sequence alignment


S.tuberosum      MADLNPFDLLGDDDNDDPSKLIAIHQQKVDPAKRASAPAAAAAKKQPAKLPTKPPPPTQA 60
A.thaliana       MATLNPFDLL-DDDAEDPS-QLAVAIEKIDKSKKSGQVSSLPAKSAP-KLPSKPLPPAQA 57
                 ** ******* *** :***  :*:  :*:* :*::.  :: .**. * ***:** **:**

S.tuberosum      VREAKTEFGRGGGRGGGRGYSRGRGGGGFNREASNNENFSRNREFSG--GIAAPEYMEGG 118
A.thaliana       VREARSDAPRGGG--GRGGFNRGRG--GYNRDDGNNGYSGGYTKPSGEGDVSKSSYERRG 113
                 ****:::  ****  *  *:.****  *:**: .**   .   : **  .:: ..* . *

S.tuberosum      RPSERRGGYGGP-HAFRGGRPGGFGNEEMPEGDRPRRTFERRSGTGRGNEIKREGAGRGN 177
A.thaliana       GGGAPRGSFRGEGGGPGGGRRGGFSNEGG-DGERPRRAFERRSGTGRGSDFKRDGSGRGN 172
                   .  **.: *   .  *** ***.**   :*:****:**********.::**:*:****

S.tuberosum      WGTEADEVTQMTGEVADEGEKNLNVEKPSTEEEAGDDKKENPAAEAEDKEPEDKEMTLEE 237
A.thaliana       WGTPGEEIAAETEAVAGVETEKDVGEKPAVDDVAADANKED--TVVEEKEPEDKEMTLDE 230
                 *** .:*::  *  **.   ::   ***:.:: *.* :**:  : .*:**********:*

S.tuberosum      YEKLLEEKRKALQALKTEERKVDTKVFESMQQIS-KKPSDEIFVKLGS-KDKRKESAEKE 295
A.thaliana       YEKILEEKKKALQSLTTSERKVDTKVFESMQQLSNKKSNDEIFIKLGSDKDKRKD--DKE 288
                 ***:****:****:*.*.**************:* **..****:**** *****:  :**

S.tuberosum      EKAKKAVSINEFLKPAEGERYYAPGGRGRGRGRGSRG--YSGANTMSNVEAAPPIEDPGH 353
A.thaliana       EKAKKAVSINEFLKPAEGGNYYRGGRGGRGRGGRGRGGVSSGESGGYRNEAAPAIGDAAQ 348
                 ****************** .**  *  *****  .**   ** .   . ****.* *..:

S.tuberosum      FPTLGGK 360
A.thaliana       FPSLGGK 355
                 **:****
```

Figure S1. Alignment of deduced RGGA protein sequences of *S. tuberosum* and *A. thaliana*. The alignment was performed using ClustalW (http://www.genome.jp/tools/clustalw/). Asterisks indicate the presence of identical aminoacids in the two aligned sequences, whereas ":" or "." indicate conserved or semi-conserved substitutions, respectively.

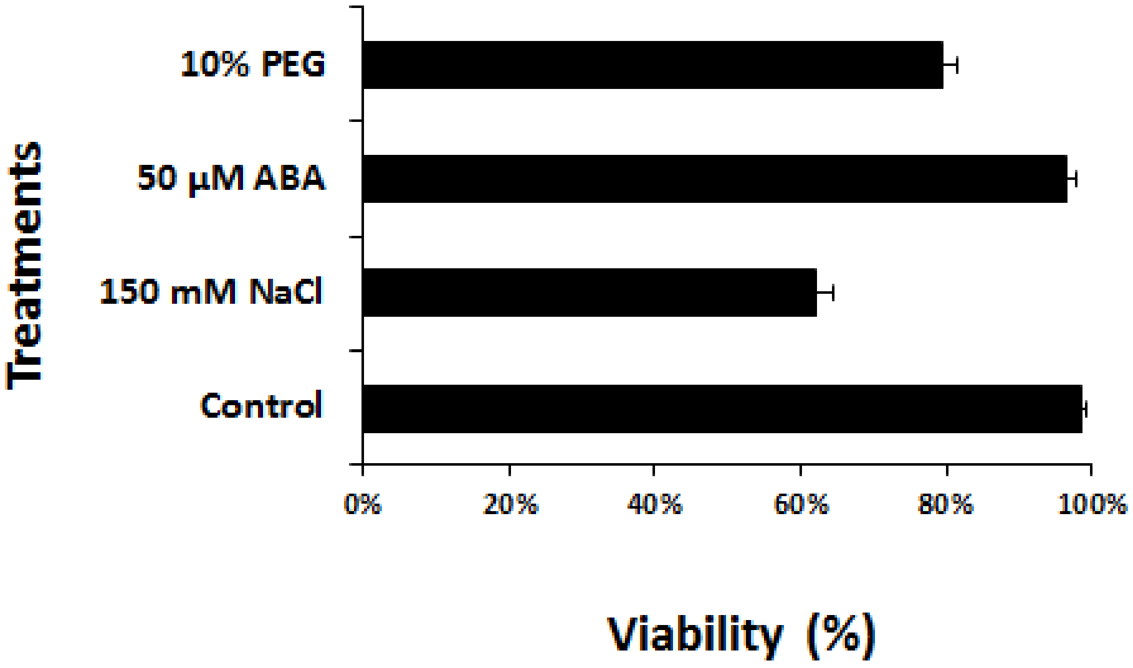

Figure S2. Cell viability measured as percentage of Arabidopsis MM2D cells in control conditions or after a 24h exposure to treatments as indicated in figure.

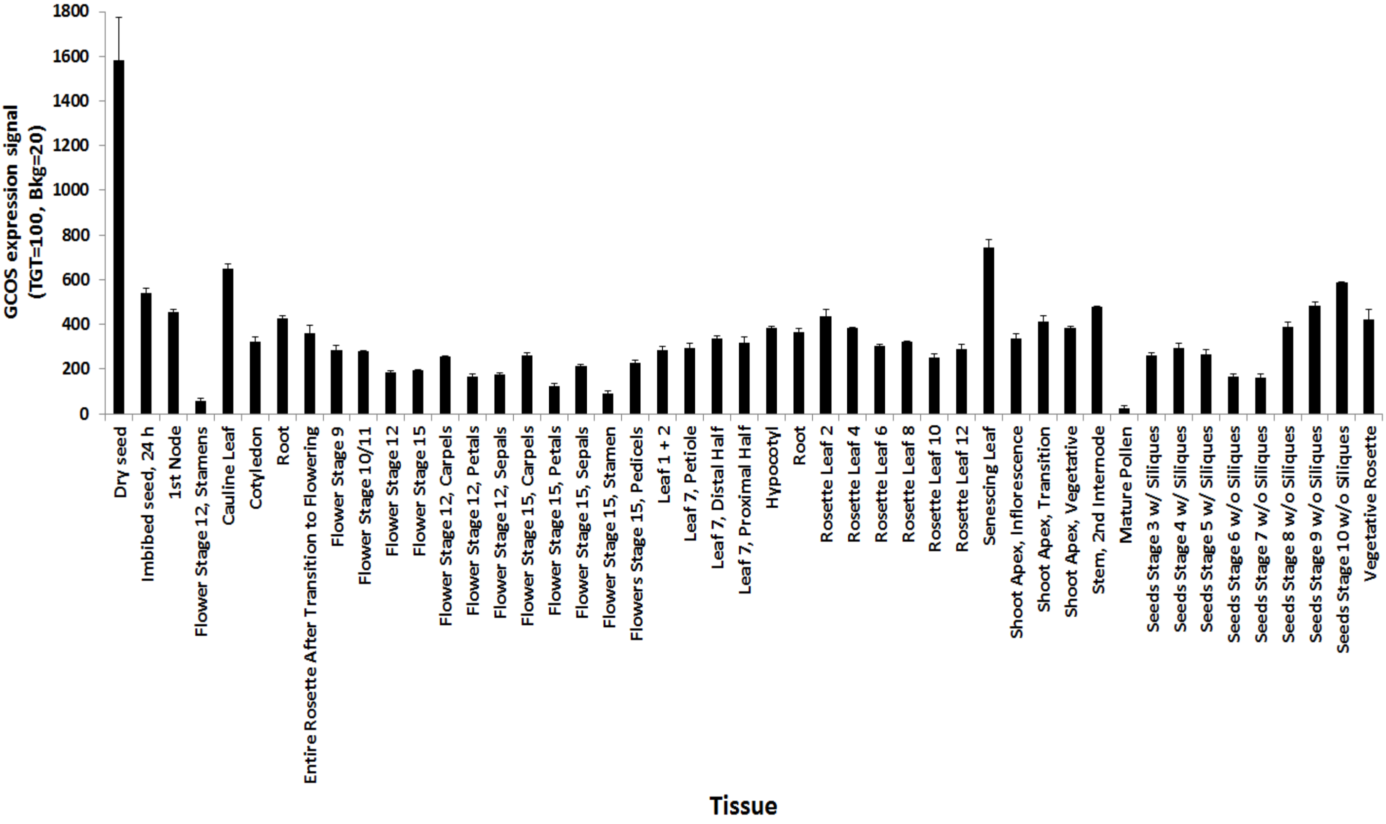

Figure S3. *AtRGGA* gene expression in different tissues and developmental stages of Arabidopsis. ATH1 microarray data were gathered and processed using the eFP browser (Winter et al., 2007). Expression signals were generated by the eFP browser using the Gene Chip Operating Signal (GCOS) using target intensity (TGT) and background (bkg) values as indicated in figure.

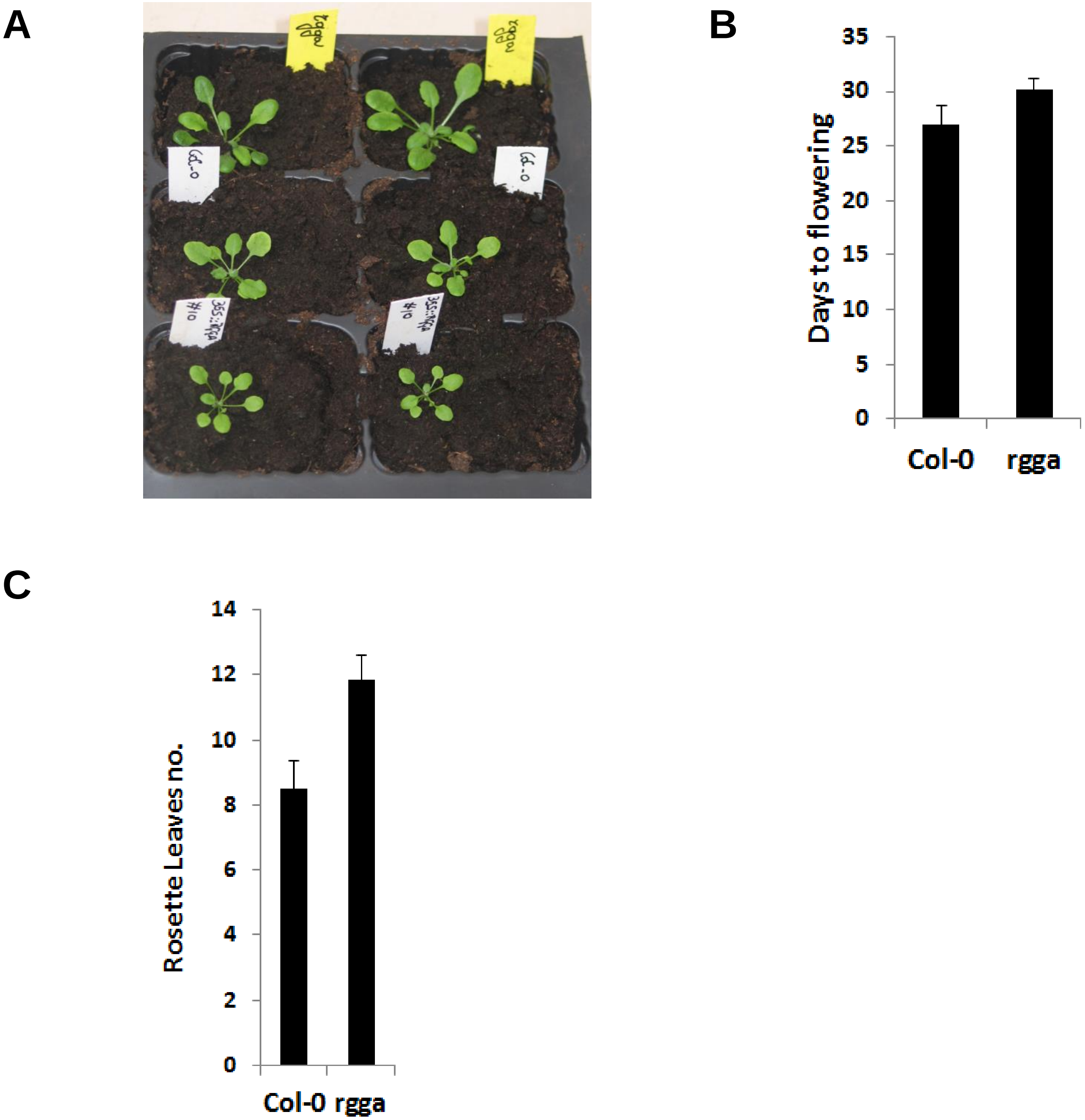

Figure S4. Phenotypes of Arabidopsis plants with modified expression of *AtRGGA*.

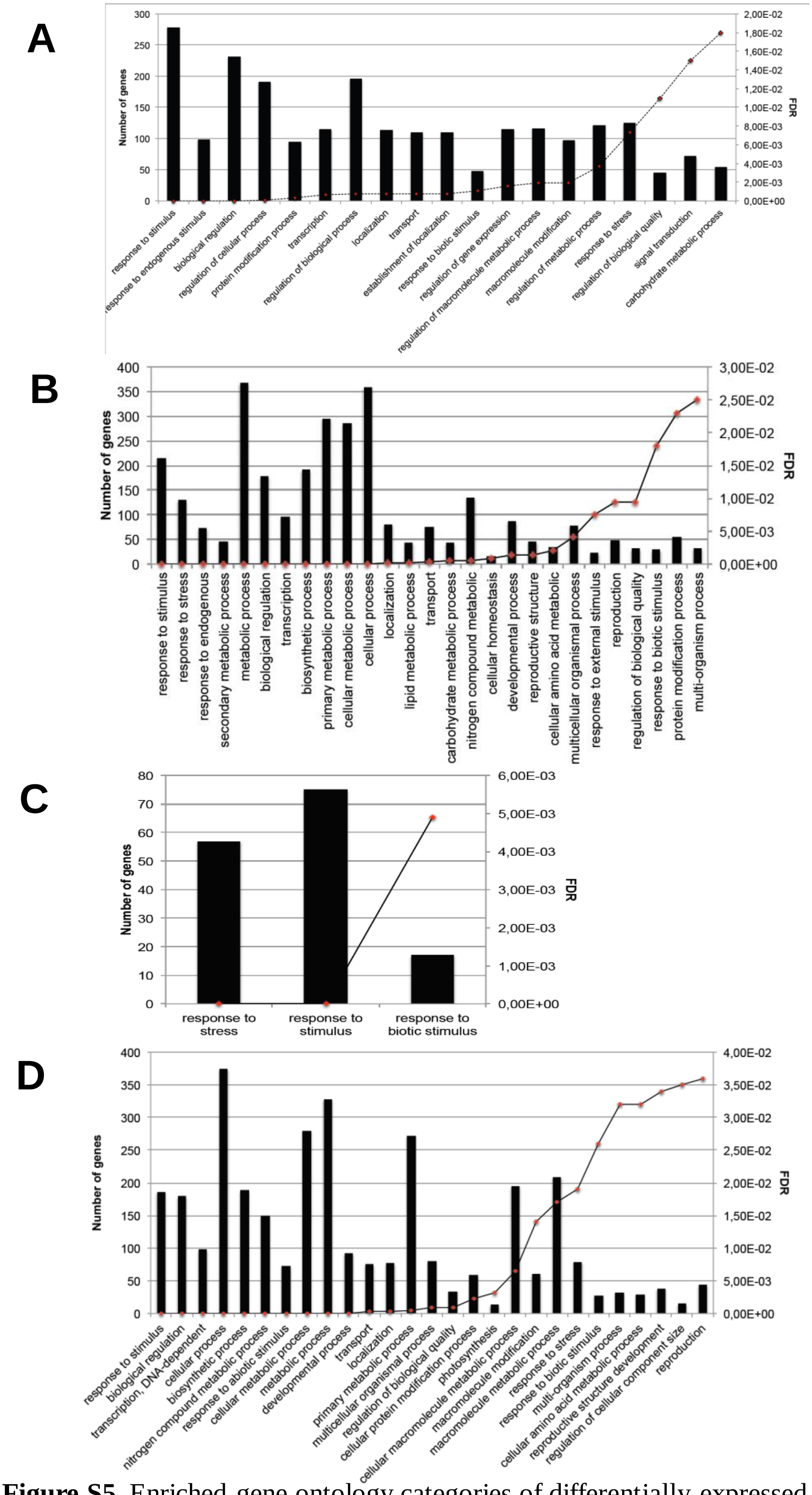

Figure S5. Enriched gene ontology categories of differentially expressed genes in 35S::FLAG-RGGA plants. (A) Enriched GO categories of up-regulated genes in control conditions; (B) Enriched GO categories of down-regulated genes in control conditions; (C) Enriched GO categories of up-regulated genes in salt stress conditions. (D) Enriched GO categories of down-regulated genes in salt stress conditions. FDR: False Discovery Rate.

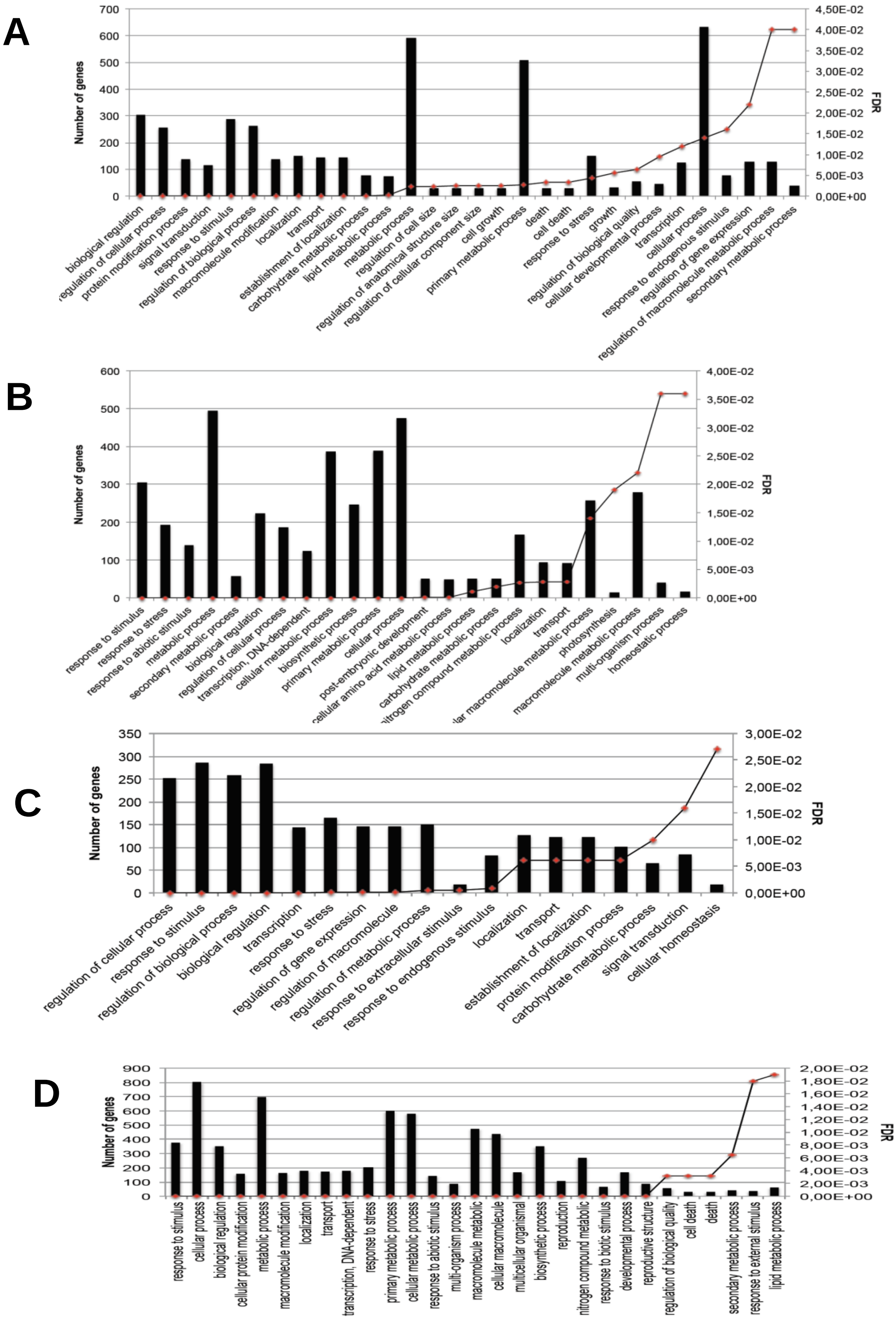

Figure S6. Enriched gene ontology categories of differentially expressed genes in *rgga* plants. (A) Enriched GO categories of up-regulated genes in control conditions; (B) Enriched GO categories of down-regulated genes in control conditions; (C) Enriched GO categories of up-regulated genes in salt stress conditions; (D) Enriched GO categories of down-regulated genes in salt stress conditions. FDR: False Discovery Rate.

Table S1. Primers used in this study

Primer Name	Sequence (5'-3')	Application
StRGGA FOR	CGTAGTGGAACTGGCAGAGG	qRT-PCR, potato
StRGGA Rev	CCAAGAGATGGGAACTGAGC	qRT-PCR, potato
StElong fact F	TGTCAAGCAAATGATCTGCTGC	qRT-PCR, potato
StElong fact R	AAGAGCGTCAAGAAGGGTTGG	qRT-PCR, potato
CYP707A2 For	TGGCTACTTGATCCCAAAGG	qRT-PCR, Arabidopsis
CYP707A2 Rev	TAAGGTTTTGGTGCCACCTC	qRT-PCR, Arabidopsis
DIN2 For	ATGACAACGACGACGGTACA	qRT-PCR, Arabidopsis
DIN2 Rev	TACGTCACACCCATCTTCCA	qRT-PCR, Arabidopsis
PAP14 For	CAGACGTTTCACCTGCAGAA	qRT-PCR, Arabidopsis
PAP14 Rev	CGTCACTTGTCTCGCACAAT	qRT-PCR, Arabidopsis
AT4G34790 For	AGGTCACGTAGCGGTTTACG	qRT-PCR, Arabidopsis
AT4G34790 Rev	CGTCAAGCCACCCATAGAGT	qRT-PCR, Arabidopsis
Dorm_For	GCGTAAGGAAAACGTGTGGA	qRT-PCR, Arabidopsis
Dorm_Rev	GTGGGAGAGTTTGGGTGAGA	qRT-PCR, Arabidopsis
HSP70 For	GGACAACAACCTCCTCGGTA	qRT-PCR, Arabidopsis
HSP70 Rev	CAGTGGTCTTGTCCTCAGCA	qRT-PCR, Arabidopsis
AAC1 For	TGCTGCTCCTATTGAACGTG	qRT-PCR, Arabidopsis
AAC1 Rev	TGCCGAAACAGTCACCAATA	qRT-PCR, Arabidopsis
bHLH119 For	AACCAGCCAACCACAAAGAC	qRT-PCR, Arabidopsis
bHLH119 Rev	GGAAGGGGAGCATTTTCTTC	qRT-PCR, Arabidopsis
AtEF-1 For	TGAGCACGCTCTTCTTGCTTTCA	qRT-PCR, Arabidopsis
AtEF-1 For	GGTGGTGGCATCCATCTTGTTACA	qRT-PCR, Arabidopsis
Rgga Fw Sal I	ACGCGTCGACAGATGGCAACTTTGAACCCTTTTG	Cloning in pET28a
Rgga Rev NotI	ATAAGAATGCGGCCGCCTTGCCCCCAAGAGATGG	Cloning in pET28a
SALK143514_LP	CCTCCTTGTTAGCATCAGCAG	T-DNA Insertion confirmation
SALK143514_RP	TCACCAACCAACAAGTTCTCC	T-DNA Insertion confirmation
LBa1	TGGTTCACGTAGTGGGCCATCG	T-DNA Insertion confirmation
RGGA For	ATGGCAACTTTGAACCCTTT	RT-PCR to detect presence of RGGA transcript
RGGA Rev	TTACTTGCCCCCAAGAGATGG	RT-PCR to detect presence of RGGA transcript
ATTrggaFor	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCAACTTTGAACCCTTT	Cloning in pDONR207
ATTrggaRev STOP	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTACTTGCCCCCAAGAGATGG	Cloning in pDONR207
ATTrggaRev NO STOP	GGGGACCACTTTGTACAAGAAAGCTGGGTCCTTGCCCCCAAGAGATGG	Cloning in pDONR207
ATTb1promsa	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGATTTATTAAAGAAAAAAGATTTG	RGGA Promoter cloning in pDNOR207
ATTb2promsa	GGGGACCACTTTGTACAAGAAAGCTGGGTCATCTTAAAACAATCCAAGTGATTAA	RGGA Promoter cloning in pDNOR207

Table S2. qRT-PCR validation of microarrays

Gene Name	Locus	Genotype/Treatment	Regulation	Fold-change (Microarrays)	Fold-change (qRT-PCR)	p value (qRT-PCR)
SAUR3	At4g34790	rgga/0 NaCl	Up	12.94	28	0.0185
PAP14	At2g46880	rgga/180mM NaCl	Up	86.54	198	0.0019
DRM2	At2g33830	35S::RGGA/0 NaCl	Up	2.59	3.95	0.1074
CYP707A2	At2g29090	rgga/0 NaCl	Down	-56.14	-5.55	0.0011
HSP70-2	At5g02490	35S::RGGA/ 0 NaCl	Down	-3.06	-2.38	0.0003
CYP707A2	At2g29090	35S::RGGA/ 180mM NaCl	Down	-34.41	-4.16	0.0146
bHLH119	At4g28811	35S::RGGA/ 180mM NaCl	Up	10.79	2.55	0.0218